

GenCore version 5.1.6
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OM protein - protein search, using sw model

Title: US-09-508-849a-17

Perfect score: 1523

Sequence: 1 MQQPFPNYPYPOQIYWVDSASS.....SELSLYNFEESQTFGLYKL 281

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1523	100.0	281	1 TNF6_HUMAN	P48023 homo sapien
2	1473.5	96.7	280	1 TNF6_CERTO	09bdnl cercocebus
3	1469.5	96.5	280	1 TNF6_MACMU	09my16 macaca mula
4	1295.5	85.1	282	1 TNF6_PIG	Q9beab sus scrofa
5	1156	75.9	279	1 TNF6_MOUSE	P41047 mus musculus
6	1136.5	74.6	278	1 TNF6_RAT	P36940 rattus norvegicus
7	250	16.4	239	1 TN14_MOUSE	Q9qyq9 mus musculus
8	224.5	14.7	240	1 TN14_HUMAN	Q43557 homo sapien
9	205	13.5	202	1 TNFB_RAT	Q06332 rattus norvegicus
10	204	13.4	202	1 TNFB_MOUSE	P09225 mus musculus
11	202.5	13.3	205	1 TNFB_MARMO	Q9Jm09 marmosaparvirostris
12	200.5	13.2	201	1 TNFB_MACMU	Q9Xt48 macropus eugenii
13	200.5	13.2	291	1 TN10_MOUSE	P50592 mus musculus
14	200	13.1	197	1 TNFB_RABBIT	P10154 oryctolagus cuniculus
15	193.5	12.7	174	1 TN15_HUMAN	Q95150 homo sapien
16	191	12.5	205	1 TNFB_HUMAN	P01374 homo sapien
17	189	12.4	317	1 TN11_HUMAN	Q14788 human tumor necrosis factor receptor type I
18	186.5	12.2	234	1 TNFA_HORSE	R29553 equus caballus
19	186	12.2	233	1 TNFA_TURTR	Q9ba21 turdus tristis
20	186	12.2	281	1 TN10_HUMAN	P50591 homo sapien
21	185.5	12.2	232	1 TNFA_PIG	P23563 sus scrofa
22	185	12.1	233	1 TNFA_DBELLE	Q8wrr1 delphinapterus leucas
23	184	12.0	204	1 TNFB_BOVIN	P26445 bos taurus
24	183.5	12.0	233	1 TNFA_CAVPA	Q065600 bovis taurus
25	183	12.0	272	1 TNF5_CHICK	Q9188 gallus gallus
26	183	12.0	272	1 TNFA_HUMAN	P01375 homo sapien
27	181	11.9	233	1 TNFA_MARMO	Q35734 marmosaparvirostris
28	180	11.8	233	1 TNFA_TRIUV	P79374 trichosurus vulpecula
29	178	11.7	233	1 YPRO_OWEFU	P21260 owenia fusiformis
30	177	11.6	141	1 YPRO_CAFNA	P51742 canis familiaris
31	176	11.6	233	1 TNFA_PAPSP	P33620 papio sp. (elaphinus)
32	176	11.6	233	1 TNFA_CEREL	P51743 cervus elaphus
33	175.5	11.5	229		

ALIGNMENTS

RESULT 1		TNF6_HUMAN		STANDARD; PRT; 281 AA.	
ID	TNF6_HUMAN	AC	P48023; Q9BZP9;	DT	01-FEB-1996 (Rel. 33, Last sequence update)
MDLINE	95127560; PubMed-782647;	DT	15-JUN-2002 (Rel. 41, Last annotation update)	DE	Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
NAME	"Human Fas ligand: gene structure, chromosomal location and species specificity"; Int. Immunol. 6:1567-1574(1994).	DE	(Apoptosis antigen ligand) (APFL) (CD178 antigen).	GN	TNFSF6 OR FASL OR APRILGI.
ORGANISM	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo sapiens (Human).	OS		RA	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo sapiens (Human).
COMMENT		RA		RT	"Fas ligand mediates activation-induced cell death in human T lymphocytes." J. Exp. Med. 181:71-77(1995).
EXPERIMENTAL		RL		RN	[2]
SEQUENCE	SEQUENCE FROM N.A. (ISOFORM 1); MEDLINE=95127560; PubMed-782647;	RP		RP	SEQUENCE FROM N.A. (ISOFORM 1); MEDLINE=95127560; PubMed-782647;
STRUCTURE	Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.: "Human Fas ligand: gene structure, chromosomal location and species specificity"; Int. Immunol. 6:1567-1574(1994).	RA		RA	Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.: "Human Fas ligand: gene structure, chromosomal location and species specificity"; Int. Immunol. 6:1567-1574(1994).
FUNCTION	SEQUENCE FROM N.A. (ISOFORM 1); MEDLINE=95071350; PubMed-7980502; Mita E., Hayashi N., Ito S., Takehara T., Hijioka T., Kasahara A., Schaezlein C.E., Pfehlmann P., Eibel R.: Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.	RA		RA	SEQUENCE FROM N.A. (ISOFORM 1); MEDLINE=95071350; PubMed-7980502; Mita E., Hayashi N., Ito S., Takehara T., Hijioka T., Kasahara A., Schaezlein C.E., Pfehlmann P., Eibel R.: Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
ROLE	"Role of Fas ligand in apoptosis induced by hepatitis C virus infection"; Biochem. Biophys. Res. Commun. 204:468-474(1994).	RA		RA	"Role of Fas ligand in apoptosis induced by hepatitis C virus infection"; Biochem. Biophys. Res. Commun. 204:468-474(1994).
CHARACTERIZATION	SEQUENCE FROM N.A. (ISOFORM 2); TISSUE="Leukocyte"; Zeytin A., Nagarjatti M., Nagarjatti P.S.: "Isolation and characterization of a new naturally occurring variant of human Fas ligand that is expressed only in membrane bound form."; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.	RC		RC	SEQUENCE FROM N.A. (ISOFORM 2); TISSUE="Leukocyte"; Zeytin A., Nagarjatti M., Nagarjatti P.S.: "Isolation and characterization of a new naturally occurring variant of human Fas ligand that is expressed only in membrane bound form."; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EXPRESSION	SEQUENCE FROM N.A. (ISOFORM 2); TISSUE="Leukocyte"; Zeytin A., Nagarjatti M., Nagarjatti P.S.: "Isolation and characterization of a new naturally occurring variant of human Fas ligand that is expressed only in membrane bound form."; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.	RR		RR	SEQUENCE FROM N.A. (ISOFORM 2); TISSUE="Leukocyte"; Zeytin A., Nagarjatti M., Nagarjatti P.S.: "Isolation and characterization of a new naturally occurring variant of human Fas ligand that is expressed only in membrane bound form."; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
PROTEIN	Wilkinson J.; Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.	RA		RA	Wilkinson J.; Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
PROTEIN		RT		RT	
PROTEIN		RN		RN	
PROTEIN		RP		RP	
PROTEIN		RL		RL	
PROTEIN		RN		RN	
PROTEIN		RR		RR	
PROTEIN		[6]		[6]	
PROTEIN		SEQUENCE FROM N.A. (ISOFORM 1); TISSUE="Blood"; Strasbourg R.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.			

DB	240 RSSYLGAVENLJSTDHLVNVSELVNFEEQTFEGLYKL 280
RL	Fas/Fas-ligand and co-stimulatory molecules.;"
CC	Immunogenetics 53:15-328(2001).
CC	- I - FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development.
CC	TNFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3 modulates its effects (By similarity).
CC	- I - SUBUNIT: Homotrimer (Probable).
CC	- I - SUBCELLULAR LOCATION: Type II membrane protein and secreted (By similarity).
CC	- I - PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
CC	- I - SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC	EMBL: AF244847; AAK37606.1; -.
DR	HSSP: P01375; 4TSV.
DR	InterPro: IPR003635; TNF_abc.
DR	IntePro: IPR00478; TNF_family.
DR	Pfam: PF00229; TNF; 1.
DR	PRINTS: PRO0134; TNECROSISFCT.
DR	ProDom: PD002012; TNFabc; 1.
DR	SMART: SM00207; TNF_1; 1.
DR	PROSITE: PS50049; TNF_2; 1.
DR	CYTOKINE: Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
FT	CHAIN 1 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 6, MEMBRANE FORM.
FT	CHAIN 129 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
FT	DOMAIN 1 80 CYTOLASMIC (POTENTIAL). SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
FT	DOMAIN 81 101 EXTRACELLULAR (POTENTIAL).
FT	DOMAIN 102 280 PRO-RICH.
FT	DOMAIN 45 64 POLY-PRO.
FT	SITE 128 129 CLEAVAGE (BY SIMILARITY).
FT	DISULFID 201 232 POTENTIAL.
FT	CARBONYD 183 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBONYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBONYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SEQUENCE 280 AA; 31407 MW; 729EA60067B/0398 CRC64;
QY	Query Match 96 %; Score 1473.5; DB 1; Length 280; Best Local Similarity 97.5%; Pred. No. 7.2e-94; Matches 274; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
QY	1 MQQPNNPPQYQIYWDDSSASSPPWAPPGTVLPCPTSVPRRGQRREPPPPLPPPPP 60
Db	1 MQQPNNPPQYQIYWDDSSASSPPWAPPGTVLPCPTSVPRRGQRREPPPPLPPPPP 59
QY	61 PPLPLPLPLPKKRRNHSTGCLCLMNFMLVLAVALGLGGMOLFHKLAELERESTSO 120
60	PPLPLPLPLPKKRRNHSTGCLCLMNFMLVLAVALGLGGMOLFHKLAELERESTSO 119
QY	121 MHTASSEKQIGHSPPERKEKELRVAHLTGKSNSRSMPLEWEITGYIVLGLGKKG 180
Db	120 KHTASSEKQIGHSPPERKEKELRVAHLTGKSNSRSMPLEWEITGYIVLGLGKKG 179
QY	181 LVINETGLYFWYSKYFRGSCNNPLSHKVYMRISKYPODLVMEKGKMSYCITGQMA 240
Db	180 LVINETGLYFWYSKYFRGSCNNPLSHKVYMRISKYPODLVMEKGKMSYCITGQMA 239
QY	241 RSSYLGAVENLJSTDHLVNVSELVNFEEQTFEGLYKL 281
FT	SEQUENCE FROM N.A. SPECIES=M.mulatta; TISSUE=Lymphocytes; MEDLINE=2138618; PubMed=11415135;
RC	RX
RC	RA
RC	RA
RL	Weiss W.R., Ansari A.A.;
RT	"Cloning, sequencing, and homology analysis of nonhuman primate Fas/Fas-ligand and co-stimulatory molecules.";
RL	Immunogenetics 53:315-328(2001).
RN	[1]
RP	SEQUENCE FROM N.A.
RC	RX
RC	RA
RC	RA
RL	Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RC	Kiril Y., Inoue T., Yoshino K.;
CC	Submitted (NOV-1999) to the EMBL/genBank/GenBank databases.
CC	- I - FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development.
CC	TNFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3 modulates its effects (By similarity).
CC	- I - SUBUNIT: Homotrimer (Potential).
CC	- I - SUBCELLULAR LOCATION: Type II membrane protein and secreted (By similarity).
CC	- I - PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
CC	- I - SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC	EMBL: AF244856; AAK37539.1; -.
DR	EMBL: AB035138; BA09294.1; -.
DR	EMBL: AB035139; BA09295.1; -.
DR	EMBL: AB035140; BA09296.1; -.
DR	HSSP: P01375; 4TSV.
DR	InterPro: IPR003635; TNF_abc.
DR	IntePro: IPR00478; TNF_family.
DR	Pfam: PF00229; TNF; 1.
DR	PRINTS: PRO0134; TNECROSISFCT.
DR	ProDom: PD002012; TNFabc; 1.
DR	SMART: SM00207; TNF_1; 1.
DR	PROSITE: PS50049; TNF_2; 1.
KW	CYTOKINE: Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
FT	CHAIN 1 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 6, MEMBRANE FORM.

FT	CHAIN	129	280	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
FT	DOMAIN	1	80	CYTOSPLASMIC (POTENTIAL).
FT	TRANSMEM	81	101	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
FT	DOMAIN	102	280	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	4	69	PRO-RICH.
FT	DOMAIN	45	64	POLY-PRO.
FT	SITE	128	129	CLEAVAGE (BY SIMILARITY).
FT	DISULFID	201	232	POTENTIAL.
FT	CARBOHYD	183	183	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	249	259	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	259	259	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	60	60	F > P (IN REF. 1).
FT	SEQUENCE	280 AA;	31367 MW;	F0B284D61A132EB4 CRC64;
Query Match		96.5%		Score 149.5; DB 1; Length 280;
Best Local Similarity		97.5%		Score 146.9; DB 1; Length 280;
Matches	274;	Conservative	0;	Mismatches 6; Indels 1; Gaps 1;
Qy	1	MOOPFNYYPQIYWDSASSPWPAPPGVLPCCPTSPVPRPGQRPPPPPPPLPPPPP 60		
Db	1	MQOPFNYYPQIYWDSASSPWPAPPGVLPCCPTSPVPRPGQRPPPPPPPLPPPPP 59		
61	PPAPPLPLPKERGNISTGLCLVLFMNVNVALVGIGMOLFHQKELBLRETSQ 120			
60	SPPLPLPLPKERGNHSTGLCLVLFMNVNVALVGIGMOLFHQKELBLRETSQ 119			
Oy	121	MHQASSLKKQIGHSPSPPEKEKLKVARYHLTGKSNSRSMPLWEDTYGIVLSSVVKYKG 180		
Db	120	KHTASSLERKQIGHSPSPPEKEKLKVARYHLTGKSNSRSMPLWEDTYGIVLSSVVKYKG 179		
Qy	181	LIVNETGYFWKVYFGQSCNLPLSHKVVRNSKYPQLDVMEGKMSCTTGQWMA 240		
Db	180	LIVNETGYFWKVYFGQSCNLPLSHKVVRNSKYPQLDVMEGKMSCTTGQWMA 239		
Qy	241	RSSVLGAVENFLTSADHLVNVNSELVSLVNEESEOTFFGKL 281		
Db	240	HSSVLGAVENFLTSADHLVNVNSELVSLVNEESEOTFFGKL 280		
RESULT 4				
TNF6_PIG				
ID	TNF6_PIG			STANDARD;
AC	Q9BEA8; 095N10; 095M04;			PRT; 282 AA.
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DE	Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand). TNFSF6 OR FASL.			
GN	Sus scrofa (Pig).			
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
OX	NCBI_TaxID:9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	LINEID=2132253; PubMed=11429161;			
RA	Mineta Y., Shimoi Y., Inumaru S., Mori Y.;			
RT	"Molecular cloning, characterization, and expression of porcine Fas ligand (CD95 ligand)", J. Interferon Cytokine Res. 21:305-312(2001).			
RT	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Guangxi bama miniature pig;			
RA	Zhu N., Young Y.;			
RT	"Molecular cloning and characterization of porcine Fas ligand cDNA.", Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.			
RL	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lymphoid;			
RA	Tsuyuki S., Kono M., Bloom E.T.;			
RT	"Cloning and potential utility of porcine Fas ligand: overexpression			
RT	In porcine cells Protects them from attack by human cytolytic cells.;"			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Moegi Ishiyama Y., Nakajima Y., Hoka S., Takagaki Y.;			
RT	"Porcine Fas-ligand gene: genomic sequence analysis and comparison with human gene.";			
RL	Mol. Immunol. 38:581-586(2002)			
CC	-1. FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that transduces the apoptotic signal into cells. May be involved in cyrototoxic T cell mediated apoptosis and in T cell development. TNFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6/DcR3 modulates its effects (By similarity).			
CC	-1. SUBUNIT: Homotrimer (Probable).			
CC	-1. SUBCELLULAR LOCATION: Type II membrane protein and secreted (By similarity).			
CC	-1. INDUCTION: By IL-18.			
CC	-1. PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).			
CC	-1. SIMILARITY: BLONDES TO THE TUMOR NECROSIS FACTOR FAMILY.			
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CC	--			
DR	AB027397; BAB4019.1; -			
DR	EMLB; AB069764; AAK56449.1; -			
DR	EMLB; AF397407; AAK84408.1; -			
DR	EMLB; AB069764; BAB64291.1; -			
DR	EMBL; AP033634; AAK56449.1; -			
DR	InterPro; IPR03636; TNF_abc.			
DR	InterPro; IPR000478; TNF_family.			
DR	PRINTS; PROJ234; TNF; 1.			
DR	PRODom; PD002012; TNF_abc; 1.			
DR	SMART; SM00207; TNF; 1.			
DR	PROSITE; PS00251; TNF_1; 1.			
DR	PROSITE; PS00049; TNF_2; 1.			
KW	Cytokine: Apoptosis; transmembrane; Glycoprotein; Signal-anchor.			
FT	CHAIN	1	282	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 6, MEMBRANE FORM.
FT	DOMAIN	131	282	TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
FT	SITE	130	131	CYTOSPLASMIC (POTENTIAL).
FT	DISULFID	203	234	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
FT	CARBOHYD	185	185	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	251	251	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	261	261	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFFLICT	5	5	F > L (IN REF. 4).
FT	CONFFLICT	57	57	T > P (IN REF. 2).
SO	SEQUENCE	282 AA;	31756 MW;	F6743DRA1145671FB CRC64;
Query Match		85.1%		Score 1295.7; DB 1; Length 282;
Best Local Similarity		85.5%		Score 1295.5; DB 1; Length 282;
Matches	242;	Conservative	14;	Mismatches 24; Indels 3; Gaps 2;
Qy	1	MOOPFNYYPQIYWDSASSPWPAPPGVLPCCPTSPVPRPGQRPPPPPLPPPP-- 58		
Db	1	MQOPFNYYPQIYWDSASSPWPAPPGVLPCCPTSPVPRPGQRPPPPPLPPPP-- 59		

QY	59	PPPLPDPPLPLPKKRGHNSGICLGLMMFFMVLVALVGLGLMFOLFHQELAELREST	118	RP CHARACTERIZATION OF VARIANT GLD.
Db	60	PSRPLPPLPPSLKKRRDHNAAGLCLLVMFFMVLVALVGLGLMFOLFHQELTELESA	119	RX MEDLINE=96091792; PubMed=7495745;
QY	119	SOMHTTASSLEQIGHSPPPKKEKLKVAHITGKSNSRSMPLEWEDTYGTWLGSYKK	178	RA Hahn M., Peitsch M.C., Immler M., Schroeter M., Lowin B., Rousseau M., Bron C., Renno T., French L., Tschopp J.; Int. Immunol. 7:1381-1386(1995).
Db	120	SQRHTTSSLEQIGHSPPPKKEKLKVAHITGKSNSRSMPLEWEDTYGTWLGSYKK	179	RL [7] RN [7]
QY	179	GGLVINITGLPFYISKVYFRGOSCNMLPLSKVYMRNSKIPQDLVMEGKAMSYCTGQM	238	RP VARIANTS ALA-184 AND GLY-218.
Db	180	GSIVVNGAVENLTSADHLYNVNSELSLVNFBESQTPFGLKL	281	RC STRAIN=various;
QY	239	WARSYVLAGAVENLTSADHLYNVNSELSLVNFBESQTPFGLKL	282	RX PubMed=9108079;
Db	240	WARSYVLAGAVENLTSADHLYNVNSELSLVNFBESQTPFGLKL	282	CC Proc. Natl. Acad. Sci. U.S.A. 94:3914-3919(1997).
RESULT	5	TNF6_MOUSE STANDARD:	PRT; 279 AA.	-I FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development. TNFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6/DcR3 modulates its effects (by similarity).
ID	TNF6_MOUSE	AC P41047; 051217; Q9RF2;	DT 01-FEB-1995 (Rel. 31, Created)	CC SUBUNIT: HOMOTRIMER (PROBABLE).
DE	Tumor necrosis factor ligand superfamily member 6 (FAS antigen	DT 01-FEB-1995 (Rel. 31, Last sequence update)	CC SECRETED (Isoforms FASL and FASLS).	
GN	TNFSF6 OR FASL OR APRILG1 OR GLD.	DT 15-JUN-2002 (Rel. 41, Last annotation update)	CC ALTERNATIVE PRODUCTS: 2 ISOFORMS: FASL (SHOWN HERE) AND FASLS ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORM FASL MEDIATES APOPTOSIS WHILE ISOFORM FASLS PREVENTS APOPTOSIS INDUCED BY FAS/FASL.	
OS	Mus musculus (Mouse)	RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G., Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	CC INTERACTION:	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OX NCBI-TaxID=10090;	RA Suda T., Nagata S.; RT "Generalized lymphoproliferative disease in mice, caused by a point mutation in the Fas ligand."; RN [1] SEQUENCE FROM N.A. (ISOFORM FASL). MEDLINE=94185175; PubMed=75111063;	CC -I PTM: The soluble form derives from the membrane form by proteolytic processing (by similarity).	
RX	RX Peitlich M.J., Tschopp J.J.; "Comparative molecular modelling of the Fas-ligand and other members of the TNF family"; Mol. Immunol. 32:761-772(1995).	RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E., RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.; RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a TNF family gene cluster."; RT Immunity 1:131-136(1994).	CC -I DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERALIZED LYMPHOPROLIFERATION DISEASE (GLD), AN AUTOSOMAL RECESSIVE DISEASE RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION.	
RN	RN [3] SEQUENCE FROM N.A. (ISOFORM FASL).	RA DR Tissue 76:969-976(1994).	CC -I SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.	
RL	RL SEQUENCE FROM N.A. (ISOFORM FASL).	RA DR EMBL; U06948; AAA17800; 1; -.	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
RN	RN SEQUENCE FROM N.A. (ISOFORM FASL).	DR DR EMBL; U10984; AAA19788; 1; -.	CC -----	
RP	RP SEQUENCE FROM N.A. (ISOFORM FASL).	DR DR EMBL; S76752; AAB33780; 1; -.	CC -----	
RX	RX MEDLINE=9519605; PubMed=78899405;	DR DR EMBL; U58959; AAB02915; 1; -.	CC -----	
RA	RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E., RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.; RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a TNF family gene cluster."; RT Immunity 1:131-136(1994).	DR DR EMBL; AF119335; AAD32106.1; -.	CC -----	
RN	RN [4] SEQUENCE FROM N.A. (ISOFORM FASL).	DR DR EMBL; U10984; AAA19788; 1; -.	CC -----	
RP	RP SEQUENCE FROM N.A. (ISOFORM FASL).	DR DR EMBL; U58959; AAB02915; 1; -.	CC -----	
RC	RC STRAIN=BALB/c;	DR DR SMART; SM02027; TNF; 1.	CC -----	
RX	RX Fanner M.H., Shioda T., Isseibacher K.J.; RT "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in two amino acids."; RT Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.	DR DR PROSITE; PS50049; TNF_2; 1.	CC -----	
RL	RL [5] SEQUENCE FROM N.A. (ISOFORM FASL).	DR DR PROSITE; PS500251; TNF; 1.	CC -----	
RN	RN STRAIN=C3H; TISSUE=Spleen;	DR DR CHAIN	CC -----	
RP	RP MEDLINE=20021634; PubMed=10552956; Ayroldi E., D'Adamo F., Zollo O., Agostini M., Moraca R., Cannarile L., Migliorati G., Delfino D.V., Riccardi C.; RT "Cloning and expression of a short Fas ligand: A new alternatively spliced product of the mouse Fas ligand gene."; RT Blood 94:3456-3467(1999).	FT FT DOMAIN	CC -----	
RC	RC	FT FT DOMAIN	CC -----	
RX	RX	FT FT DOMAIN	CC -----	
RA	RA	FT FT DOMAIN	CC -----	
RA	Ayroldi E., D'Adamo F., Zollo O., Agostini M., Moraca R., Cannarile L., Migliorati G., Delfino D.V., Riccardi C.; RT "Cloning and expression of a short Fas ligand: A new alternatively spliced product of the mouse Fas ligand gene."; RT Blood 94:3456-3467(1999).	FT FT DOMAIN	CC -----	
RN	[6]	FT FT DISULFID	CC -----	
		FT FT CARBOHYD	CC -----	

OC Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi; OX Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus; RN Mammalia; Bivalvia; Gastropoda; Cephalopoda; Ctenophora; RT Ctenophora; NCBI_TaxID=10090; RP Published=20070230; SEQUENCE FROM N.A. [1] RT Tissue=Rat; RA Tamada K., Shimozaki K., Chapoval A.I., Zhu G., Sica G., Flies D., Boone T., Hsu H., Fu Y.-X., Nagata S., Ni J., Chen L.; RT "Modulation of T-cell-mediated immunity in tumor and graft-versus-host disease models through the LIGHT co-stimulatory pathway."; Nat. Med. 6:283-289(2000). [2] RN SEQUENCE FROM N.A. RT Tissue=Fetal liver; RC Misawa K., Nasaka T., Kitamura T., Kojima T.; RT "Murine LIGHT, a homologue of human LIGHT which is a member of TNF family;" Submitted: (JUN-1999) to the EMBL/genBank/DDBJ databases. [3] RP SEQUENCE FROM N.A. RC TISSUE=Lymphoma; RA Force W.R., Todd P.K., Mikayama T.; RT "Mouse LIGHT: molecular genetics, ligand binding and expression."; Submitted (JAN-2000) to the EMBL/genBank/DDBJ databases. RL -I- FUNCTION: Cytokine that binds to TNFRSF3/LTBR. Binding to the decoy receptor TNFRSF6B modulates its effects. Activates NFkB and stimulates the proliferation of T cells. CC -I- SUBUNIT: Homotrimer (By similarity). CC -I- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By similarity) CC -I- PIM: The soluble form derives from the membrane form by proteolytic processing. CC -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY. CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by commercial entities requires a license agreement. (See <http://www.ebi.ac.uk/announce/> or send an email to license@ebi.ac.uk). DR EMBL; AF123385; AAH76453; 1; -; CC EMBL; AB029155; BAAB88559; 1; -; CC EMBL; AP22753; AFM36722; 1; -; CC HSSP; P01375; 4TSV. DR MGD; MGI:1135517; Tnfsf14. DR Interpro; IPR003636; TNF_abc. DR Interpro; IPR00478; TNF_family. DR PFAM; PF00229; TNF_1. DR PRINTS; PRO1234; TNECROSISFCT. DR PRODOM; PD002012; TNF_abc; 1. DR SMART; SM00207; TNF_1. DR PROSITE; PS00251; TNF_1; FALSE_NEG. DR PROSITE; PS50049; TNF_2; 1. DR CYTOKINE; CYTOKIN; Transmembrane; glycoprotein; signal-anchor. CHAIN 1 239 TUMOR_NECROSIS_FACTOR_LIGAND_SUPERFAMILY MEMBER 14, MEMBRANE FORM. FT DOMAIN 782 239 TUMOR_NECROSIS_FACTOR_LIGAND_SUPERFAMILY MEMBER 14, SOLUBLE FORM. FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL). FT TRANSMEM 38 58 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN) (POTENTIAL). FT DOMAIN 59 239 EXTRACELLULAR (POTENTIAL). FT SITE 81 82 CLEAVAGE (POTENTIAL). FT DISULFID 152 187 POTENTIAL. FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL). FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL). SEQUENCE 239 AA; 26338 MW; 217874ACT71AD6BB3 CRC64; SQ Q4YQKPKRKKHNSHGTLGLCLVMFFNVALVGLGID--GMFOQLHLOKELAEL-----RE 177 SWKL-----IQDQRSHQANP-----AAHLTGANSALIGIGGLPLWTRGLAFLRG 1 DB 18 IPFRRLQEONRRRRCGTVQOVSIALVLLGAGIATOWFW-LLRHQHGDIVAHLPDGKG 7 QY 117 STSQMITTASSLEKQIIGHSPPEKKELRKVHLTGNSNR---SMLEWEDTYGVLLSG 1 DB 77 SWKL-----IQDQRSHQANP-----AAHLTGANSALIGIGGLPLWTRGLAFLRG 1 QY 174 VVKKGGLVNVNTGFLGVFSKYFQOSC----NNPLSLRKVYMNNSKFPQLVMEGR 2 RN 124 LYHDGALVTPMPEGVYVWSVQLSGVGCPQGLANGLPIPTGGLYKRTSRPKKELELVSR 1 QY 229 MNSYC--TNQGWMASSYLGAVENITSDAHLVYVNESELVNFEE-SOFTGFLY 279 DB 184 -RSPCGRANSSRVWWDSSFLGGVVHLEAGEEVVVRVPGNRLVRPRDGTRSYFGAF 237

RESULT 8
TN14_HUMAN
 ID TN14_HUMAN STANDARD; PRT; 240 AA.
 AC 043557; O75476; Q8WVF6;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 15-OCT-2001 (Rel. 40; Last sequence update)
 DT 15-JUN-2002 (Rel. 41; Last annotation update)
 DE tumor necrosis factor ligand superfamily member 14 (Herpesvirus entry mediator-ligand) (HVEM-L).
 DE TNFSF14 OR LIGHT OR HVEM-L.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo. OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=9812230; PubMed=946508;
 RA Mauri D.N., Ebner R., Montgomery R.T., Kochel K.D., Cheung T.C., Yu G.-L., Ruben S., Eisenberg R.J., Cohen G.H., Spear P.G., Ware C.F.;
 RA "LIGHT, a new member of the TNF superfamily, and lymphotoxin alpha are ligands for herpesvirus entry mediator.";
 RT Immunity 8:21-30(1998).
 RL [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
 RC TISSUE=Liver;
 RX MEDLINE=9443852; PubMed=9765587;
 RA Harrop J.A., Macdonell P.C., Brigham-Burke M., Lyn S.D., Minton J., Tan K.B., Debe K., Spampinato J., Silverman C., Hensley P., DiPrinzio B.R., Emery J.G., Deen K., Eichman C., Chabot-Fletcher M., Truneh A., Young P.R.;
 RA "Herpesvirus entry mediator ligand (HVEM-L), a novel ligand for HVEM/TR2, stimulates proliferation of T cells and inhibits HIV-2 cell growth.";
 RL [3] J. Biol. Chem. 273:27548-27556(1998).
 RN SEQUENCE FROM N.A. (ISOFORM 2), AND PROCESSING.
 RX MEDLINE=21528948; PubMed=11673523;
 RA Granger S.W., Butrovich K.D., Houshmand P., Edwards W.R., Ware C.F.;
 RT "Genomic characterization of LIGHT reveals linkage to an immune response locus on chromosome 19p13.3 and distinct isoforms generated by alternate splicing or proteolysis.";
 RT RL J. Immunol. 167:5122-5128(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
 CC -I- FUNCTION: Cytokine that binds to TNFRSF3/LTBR. Binding to the decoy receptor TNFRSF6B modulates its effects. Activates NFkB, stimulates the proliferation of T cells, and inhibits growth of the adenocarcinoma HT-29. Acts as a receptor for Herpes simplex virus.
 CC -I- SUBUNIT: Homotrimer.
 CC -I- SUBCELLULAR LOCATION: Type II membrane protein and secreted

RESULT 10

TNFB_MOUSE	STANDARD;	PRT:	202 AA.
ID	TNFB_MOUSE		
AC	P09275;		
DT	01-MAR-1989 (Rel. 10, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Lymphotoxin-alpha precursor (lta-alpha) (TNF-beta) (Tumor necrosis factor ligand superfamily member 1).		
DE	LTA OR TNFSF1 OR TNFB		
RP	Mus musculus (Mouse)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	Medline=88067722; Pubmed=3684584;		
RA	Simon D., Kawashima E., Jongeneel C.V., Shakhov A.N., Nedospasov S.A.;		
RT	"Nucleotide sequence of the murine TNF locus, including the TNF-alpha (tumor necrosis factor) and TNF-beta (lymphotoxin) genes.";		
RL	Nucleic Acids Res. 15:9083-9084(1987).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	Medline=87040736; Pubmed=3490653;		
RA	Nedospasov S.A., Hart B., Shakhov A.N., Dobrynin V.N., Kawashima E.,		
RT	"The genes for tumor necrosis factor (TNF-alpha) and lymphotoxin (TNF-beta) are tandemly arranged on chromosome 17 of the mouse.";		
RL	Nucleic Acids Res. 15:3337-3337(1987).		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RX	Medline=87231057; Pubmed=3588316;		
RA	Gray P.W., Chen E., Tang W.-L., Ruddle N.;		
RT	"The murine tumor necrosis factor-beta (lymphotoxin) gene sequence.";		
RL	Nucleic Acids Res. 15:3337-3337(1987).		
RN	[5]		
RP	SEQUENCE FROM N.A.		
RX	Medline=87224127; Pubmed=2884262;		
RA	Li C.B., Gray P.W., Lin P.F., McGrath K.M., Ruddle F.H.,		
RT	"Cloning and expression of murine lymphotoxin cDNA.";		
RL	J. Immunol. 138:4496-4501(1987).		
RN	[5]		
RP	SEQUENCE FROM N.A.		
RX	Medline=87252204; Pubmed=2883372;		
RA	Gardner S.M., Mock B.A., Hilgers J., Ruppi K.E., Roeder W.D.,		
RT	"Mouse lymphotoxin and tumor necrosis factor: structural analysis of the cloned genes, physical linkage, and chromosomal position.";		
RL	J. Immunol. 139:476-483(1987).		
RN	[6]		
RP	SEQUENCE FROM N.A.		
RA	Rowen L., Qin S., Madan A., Abbas I.N., James R., Dickhoff R.,		
RA	Shaffer T., Ratcliffe A., Lotetz C., Lasky S., Hood L.,		
RT	"Sequence of the mouse major histocompatibility class III region.";		
RL	Submitted (Oct-1999) to the EMBL/GenBank/DDBJ databases.		
RN	[7]		
RP	SEQUENCE OF 6-202 FROM N.A.		
RX	Medline=891445202; Pubmed=3147435;		
RA	Well D., Dautry F.;		
RT	"Induction of tumor necrosis factor-alpha and -beta and interferon-gamma mRNA by interleukin 2 in murine lymphocytic cell lines.";		
RL	Oncogene Res. 3:409-414(1988).		
RN	[8]		
RP	SEQUENCE OF 56-76 FROM N.A.		
RX	Medline=91042516; Pubmed=1700275;		

RESULT 11

RA	Weil D., Brosset S., Dautry F.;		
RT	"RNA processing is a limiting step for murine tumor necrosis factor beta expression in response to interleukin-2.";		
RT	Mol. Cell. Biol. 10:5865-5875(1990).		
RL	-1- FUNCTION: Cytokine that in its homotrimeric form binds to TNFRSF1A/TNFRSF1B/TNFRSF1A/TNFRSF1B and TNFRSF1A/TNFRSF1B. In its heterotrimeric form with LTB binds to TNFRSF3/LTB. Lymphotoxin is produced by lymphocytes and cytotoxic for a wide range of tumor cells in vitro and in vivo		
CC	-1- SUBUNIT: Homotrimer, and heterotrimer of either two LTA and one LTB subunits or (less prevalent) two LTA and one LTB subunits (BY similarity).		
CC	-1- PROTEIN (HETEROTRIMERS) (BY SIMILARITY).		
CC	-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.		
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CC	-----		
DR	DR U05950; AAA10593; 1; --		
DR	DR Y00467; CAA6829; 1; --		
DR	DR X06217; CAA29866; 1; --		
DR	DR X06218; CAA29567; 1; --		
DR	DR Y00137; CAA68330; 1; --		
DR	DR M16319; AAA40460; 1; --		
DR	DR M17015; AAA39450; 1; --		
DR	DR AF109719; AAC024851; 1; --		
DR	DR X14300; CAA32006; 1; --		
DR	DR M60586; AAA40461; 1; --		
DR	DR B27303; B27303.		
DR	DR PIR; S01342; S01342.		
DR	DR PIR; S10083; S10083.		
DR	DR HSSP; P01374; ITNR.		
DR	DR MGII:104797; Ita.		
DR	DR InterPro; IPR003636; TNF_abc.		
DR	DR InterPro; IPR000478; TNF_family.		
DR	DR Pfam; PF00229; TNF; 1.		
DR	DR PRINTS; PR01234; TNFCROSSIFCT.		
DR	DR PRODOM; PP002012; TNF_aabc; 1.		
DR	DR SMART; SM00207; TNF; 1.		
DR	DR PROSITE; PS00251; TNF_1; 1.		
DR	DR PROSITE; PS50059; TNF_2; 1.		
DR	DR CYTOKINE; Glycoprotein; Cytotoxin; Signal.		
FT	FT SIGNAL; 1; 33		
FT	FT CHAIN; 34; 202		
FT	FT CARBOHYD; 94; 94		
FT	FT CONFLICT; 26; 26		
FT	FT CONFLICT; 161; 162		
SO	SEQUENCE 202 AA; 21998 MW; F496F83C685990D3 CRC64;		
Query	Query Match	13 48%	Score 204; DB 1; Length 202;
Best	Local Similarity	32.5%	Pred. No. 1.7e-07;
Matches	51; Conservative	25;	Mismatches 73; Indels 8; Gaps 2;
QY	133 HPSPPPERKE--LRKVAHLGKRSNSRSMPLWEDTYGVILSLGVVKGGLVINNGLYF 190		
Db	46 HPLPKKHITHGTLIKPAHLVGPSKNSLRASTDRFLRGFSISSLNLLIPPSGLYF 105		
QY	191 VYSKVVFRRGQCN-----NPLSHVYMRNSKYPDOLVMMEKGKMSYCCTGQMMARSSY 244		
Db	106 VYSQVVFSGECSRAPIPTPYLAHVQLSSQYVPHPLISAQSVVYQGLQPVRSY 165		
QY	245 LGAVFNLTSDADLYVNSLSELSLVNEFERSQFFGLYKL 281		
Db	166 OGAVFNLTKGDLSTHTDGISHLHSPPSPVFGAPAL 202		

			BEST LOCAL SIMILARITY	28.3%	PRED.	NO. 4.2e-07;	GAPS	9;
BB	POTAQHLSOKSLKRETEIKPAAHVLGDPVQD-SIHWRANTDHAFRLRGFTSLNSNLIVPT	100	MATCHES	60;	CONSERVATIVE	39;	MISMATCHES	68;
QY	TGLYFVTSKYFRGQSCNN---LILSHKYMRSNKPQDLVMMEGKMSCTTGQWMA	240	AC	103	OFLHLOKELAIRESESTQSMHRSKASLEKQIGHSPPPPEKKERLKV AHLTG--KSNSISMP	159	DB	186
Db	101 SGLYLGAVENLTSADHLVNVNSELVNFNEESQTFEGIYKL 281		AC	87	DQLQLEEVTLR--EWEDT-YGTLLSGVKYKGGLVNTETGIGLYFVSYRVQGSCNNL	205	Db	241 RSYVQGAVFLQGDLSTYDGVSHLQSFSVFGAFAL 201
QY	161 RSVYQGAVFLQGDLSTYDGVSHLQSFSVFGAFAL 201		AC	144	LSKDGTKLQKIESWESSRKHSPLNHLVFLRNGELVIEQEGLYVQSQTFRQEADAS	203	Db	206 -----PLSHKYMRSKYPDLVMMEGKMSCTTGQWMA-----SSVLA 247
DE	RESULT 13		AC	206	-----PLSHKYMRSKYPDLVMMEGKMSCTTGQWMA-----SSVLA 247		Db	204 RMVSKDKVRTIQQLVQTY-KTYSYPDPDVLMKSARN-----CWSRDAEGLYLSIYQGG 256
DE	TN10_MOUSE	STANDARD;	AC	204	RMVSKDKVRTIQQLVQTY-KTYSYPDPDVLMKSARN-----CWSRDAEGLYLSIYQGG 256		Db	248 VFNLTSDADHLVNVNSELVNFNEESQTFEGIYKL 279
DE	PRT;	291 AA.	AC	248	VFNLTSDADHLVNVNSELVNFNEESQTFEGIYKL 279		Db	257 LFELKNDNRIVSYVTWHELMQDQEASFFGA 288
DE	P50592;		AC	257	LFELKNDNRIVSYVTWHELMQDQEASFFGA 288		QY	QY
DE	01-OCT-1996 (Rel. 34, Created)		AC	QY	QY		QY	QY
DE	01-OCT-1996 (Rel. 34, Last sequence update)		AC	QY	QY		QY	QY
DE	Tumor necrosis factor ligand superfamily member 10 (TNF-related		AC	QY	QY		QY	QY
DE	apoptosis inducing ligand) (TRAIL protein).		AC	QY	QY		QY	QY
GN	TNFSF10 OR TRAIL.		AC	QY	QY		QY	QY
OS	Mus musculus (Mouse).		AC	QY	QY		QY	QY
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		AC	QY	QY		QY	QY
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		AC	QY	QY		QY	QY
OC	NCBI-TaxID=10090;		AC	QY	QY		QY	QY
OX	RX		AC	QY	QY		QY	QY
OX	SEQUENCE FROM N.A.		AC	QY	QY		QY	QY
RA	PUBMED=8777713;		AC	QY	QY		QY	QY
RA	MEDLINE=96111955;		AC	QY	QY		QY	QY
RA	Nicholls J.K., Schooley K.J., Smolak P.J., Din W.S., Huang C.-P.,		AC	QY	QY		QY	QY
RA	Goodwin R.G.; Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,		AC	QY	QY		QY	QY
RT	"Identification and characterization of a new member of the TNF		AC	QY	QY		QY	QY
RT	family that induces apoptosis";		AC	QY	QY		QY	QY
RL	Immunity 3:673-682(1995).		AC	QY	QY		QY	QY
CC	-!- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,		AC	QY	QY		QY	QY
CC	TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and		AC	QY	QY		QY	QY
CC	possibly also to TNFRSF1B/OPG. Induces apoptosis. Its activity		AC	QY	QY		QY	QY
CC	may be modulated by binding to the decoy receptors		AC	QY	QY		QY	QY
CC	TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF1B/OPG that cannot		AC	QY	QY		QY	QY
CC	induce apoptosis.		AC	QY	QY		QY	QY
CC	-!- SUBUNIT: Heterotrimer (By similarity).		AC	QY	QY		QY	QY
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).		AC	QY	QY		QY	QY
CC	-!- TISSUE SPECIFICITY: Widespread.		AC	QY	QY		QY	QY
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.		AC	QY	QY		QY	QY
CC	-----		AC	QY	QY		QY	QY
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CC	SEQUENCE FROM N.A.		AC	QY	QY		QY	QY
CC	PUBMED=2633043;		AC	QY	QY		QY	QY
CC	MEDLINE=91022056;		AC	QY	QY		QY	QY
CC	Shakhov A.N., Kuprash D.V., Turetskaya R.L., Azizov M.M.,		AC	QY	QY		QY	QY
CC	Andreyeva A.V., Nedospasov S.A.; "Cloning and structural analysis of genes coding for tumor necrosis factor and lymphotoxin in rabbits"; Mol. Biol. (Mosk) 23:1743-1750(1989).		AC	QY	QY		QY	QY
CC	-!- FUNCTION: Cytokine that in its homotrimeric form binds to TNFRSF1A/TRAILR1, TNFRSF1B/TRAILR2 and TNFRSF14/HVEM. In its heterotrimeric form with LTB binds to TNFRSF3/LTB. Lymphotoxin is produced by lymphocytes and cytotoxic for a wide range of tumor cells in vitro and in vivo.		AC	QY	QY		QY	QY
CC	-!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one LTA subunits or (less prevalent) two LTB and one LTA subunits (By similarity).		AC	QY	QY		QY	QY
CC	-!- SUBCELLULAR LOCATION: Secreted (homotrimer) and type II membrane protein (heterotrimers) (By similarity).		AC	QY	QY		QY	QY
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.		AC	QY	QY		QY	QY
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CC	SEQUENCE		AC	QY	QY		QY	QY

DR EMBL; M00341; AAA31485.1; -.
 DR PIR; JH0309; JH0309.
 DR PIR; PN0098; PN0098.
 DR HSSP; P01374; TNFR.
 DR InterPro; IPR003636; TNF_abc.
 DR InterPro; IPR000478; TNF_family.
 DR Pfam; PF00229; TNF_1.
 DR PRINTS; PRO1234; TNECROSISCT.
 DR PRODOM; PD003012; TNF_abc; 1.
 DR SMART; SM00207; TNF_1.
 DR PROSITE; PS50049; TNF_2; 1.
 DR PROSITE; PS50049; TNF_2; 1.
 DR CYTOKINE; Glycoprotein; Cytotoxin; Signal.
 FT SIGNAL; 1.
 FT CHAIN; 27 197 LYMPHOTOXIN-ALPHA.
 FT CARBOHYD; 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 197 AA: 21126 MW: 0CF18CC90B5E2345 CRC64;

Query Match 13.1%; Score 13.1%; DB 1; Length 197;
 Best Local Similarity 26.0%; Pred. No. 3e-07; 26.0%; Mismatches 82; Indels 64; Gaps 7; Matches 61; Conservative 28; Mismatches 82; Indels 64; Gaps 7; CC
 55 PPPPPPPPPLPPLPPLPKRKGHNHGICLLVMFMVLYALVQGLGMQFLFHQLKELAE 114
 19 PPPGAQGLPAGSEPPPSAAR----- 38
 115 RESIQMHTPASLEKQIGHPSPPKEKKERKVAHLTGKNSNSRSMPLME-DYIGIVLIG 173
 39 -----NAQORIQLKHFGST-----IKPAAHILVGDPSSAQD-SLRWRNTRDRAFTHLG 83

Qy 174 WKVKGGLVINETGLYFVSKVFRGOSCN-----NPLSHKVYMRNSKYPDLVMMEG 227
 Db 84 FSLSNNSLILVPSSGLYFVTSQWVFSGECSGPCKAVPTPLVLAHEVOLQFSSQISHPVPLSA 143

Qy 228 KMMSYCTQO-MWRSSTYGVNLTSADHLYVNVESELVNTEEESQFFGLKL 281

Db 144 Q-KSVCPGPQQPVRSVQIAGAVFLITQDQLSTHTDGIAHLLSPSSVFGAFAL 197

RESULT 15

TN15_HUMAN STANDARD; PRM; 174 AA.

ID TN15_HUMAN STANDARD; PRM; 174 AA.

AC Q05150; 1.
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 15 (Vascular endothelial cell growth inhibitor) (TNF ligand-related molecule 1).
 GN TNFSP15 OR VEG1 OR TNL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN NCBI_TaxID=9606; [1]
 RP Sequence from N.A.
 RC TISSUE-Ombilical vein;
 RX PubMed:9872342;
 RA Zhai Y., Ni J., Jiang G.-W., Lu J., Xing L., Lincoln C., Carter K.C., Janat F., Kozak D., Xu S., Rojas L., Aggarwal B.B., Ruben S., Li L.-Y., Gentz R., Yu G.-L.;
 RT & novel cytokine of the tumor necrosis factor family, is an angiogenesis inhibitor that suppresses the growth of colon carcinomas in vivo.;
 RL FASEB J. 13:181-189(1999).
 CC -I- FUNCTION: Inhibits vascular endothelial growth and angiogenesis (in vitro).
 CC -I- SUBUNIT: Homotrimer (Potential).
 CC -I- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
 CC -I- TISSUE SPECIFICITY: Specifically expressed in endothelial cells.
 CC Detected in Placenta, lung, kidney, skeletal muscle, pancreas, spleen, prostate, small intestine and colon.
 CC -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC

DR EMBL; AF03930; AAD08783.1; -.
 DR Genew; HGNC:11931; TNFSF15.
 DR PRINTS; PRO1234; TNECROSISCT.
 DR PRODOM; PD003012; TNF_abc; 1.
 DR SMART; SM00207; TNF_1.
 DR PROSITE; PS50049; TNF_2; 1.
 DR CYTOKINE; Glycoprotein; Cytotoxin; Signal.
 FT SIGNAL; 1.
 FT CHAIN; 27 197 LYMPHOTOXIN-ALPHA.
 FT CARBOHYD; 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 197 AA: 21126 MW: 0CF18CC90B5E2345 CRC64;

Query Match 12.7%; Score 193.5; DB 1; Length 174;
 Best Local Similarity 36.8%; Pred. No. 7.4e-07; 36.8%; Mismatches 49; Indels 15; Gaps 6; Matches 50; Conservative 22; CC
 TRANSMEM 13 25 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT DOMAIN 26 174 EXTRACELLULAR (POTENTIAL).
 FT DISULFID 85 125 POTENTIAL.
 FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 174 AA: 20131 MW: CCB83BA7EE673B98 CRC64;

Query Match 12.7%; Score 193.5; DB 1; Length 174;
 Best Local Similarity 36.8%; Pred. No. 7.4e-07; 36.8%; Mismatches 49; Indels 15; Gaps 6; Matches 50; Conservative 22; CC
 TRANSMEM 13 25 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT DOMAIN 26 174 EXTRACELLULAR (POTENTIAL).
 FT DISULFID 85 125 POTENTIAL.
 FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 174 AA: 20131 MW: CCB83BA7EE673B98 CRC64;

Qy 209 HKVYMR--NSKYPDLVNEKGKMSCTGOMYARRSSTYGVENLTSADHLYVNVESEL 266
 Db 100 ITVVITKVTDSYBPPTQIIMG-TKSCIEVGSNNFQPIYLGAMEFSLQEGDKLMVNSD 158

Qy 267 VNF-EESQFFGLYKL 281
 Db 159 VDVTKEDKTFGGAFLL 174

Search completed: June 24, 2003, 11:05:28
 Job time : 11.364 secs

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 CC -----
 CC EMBL; AF03930; AAD08783.1; -.
 CC Genew; HGNC:11931; TNFSF15.
 CC PRINTS; PRO1234; TNECROSISCT.
 CC PRODOM; PD003012; TNF_abc; 1.
 CC SMART; SM00207; TNF_1.
 CC PROSITE; PS50049; TNF_2; 1.
 CC CYTOKINE; Glycoprotein; Cytotoxin; Signal.
 CC SIGNAL; 1.
 CC CHAIN; 27 197 LYMPHOTOXIN-ALPHA.
 CC CARBOHYD; 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 197 AA: 21126 MW: 0CF18CC90B5E2345 CRC64;

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 CC -----
 CC EMBL; AF03930; AAD08783.1; -.
 CC Genew; HGNC:11931; TNFSF15.
 CC PRINTS; PRO1234; TNECROSISCT.
 CC PRODOM; PD003012; TNF_abc; 1.
 CC SMART; SM00207; TNF_1.
 CC PROSITE; PS50049; TNF_2; 1.
 CC CYTOKINE; Transmembrane; Glycoprotein; Signal-anchor.
 CC CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 1 12 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CC TRANSMEM 13 25 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CC FT DOMAIN 26 174 EXTRACELLULAR (POTENTIAL).
 CC FT DISULFID 85 125 POTENTIAL.
 CC FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT SEQUENCE 174 AA: 20131 MW: CCB83BA7EE673B98 CRC64;

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OM protein - protein search, using sw model

Run on: June 24, 2003, 11:01:33 ; Search time 21.3505 Seconds

Sequence: (without alignments)
1265.253 Million cell updates/sec

Title: US-09-508-849a-17
Perfect score: 1523

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 9613422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR73:*

1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

No.	Score	Query	Match	Length	DB	ID	Description
1	1523	100.0	281	2	138707		Fas ligand - human
2	1156	75.9	279	2	A53062		C;Species: Homo sapiens (man)
3	1136.5	74.6	278	2	A49266		C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
4	205	13.5	202	1	JN0869		R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.
5	204	13.4	202	1	B27303		A;Int: Immunol. 6, 1567-1574, 1994
6	200	13.1	197	1	JH0309		A;Title: Human Fas ligand: gene structure, chromosomal location and species specifici
7	191	12.5	205	1	QWHUX		A;Reference number: 138707; MUID:95127550; PMID:7826947
8	186.5	12.2	234	1	J01344		A;Accession: 138707
9	185.5	12.2	232	1	S12606		A;Status: preliminary; translated from GR/EMBL/DDJB
10	184	12.1	204	1	S17289		A;Molecule type: mRNA
11	183.5	12.0	204	1	S24641		A;Residues: 1-281 <RCS>
12	183	12.0	233	1	S24642		R;Mita, E.; Hayashi, N.; Ito, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto,
13	181	11.9	233	1	QWHUN		Biochem. Biophys. Res. Commun. 204, 468-474, 1994
14	177	11.6	141	2	A34043		A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
15	176	11.6	233	1	S22052		A;Status: preliminary; translated from GB/EMBL/DDJB
16	175	11.5	234	1	A25451		A;Molecule type: mRNA
17	172	11.3	599	2	T10798		A;Accession: J013410
18	171.5	11.3	415	1	A34170		A;Cross-references: EMBL:U08137; PIDN: AAC50071.1; PID:9136990
19	169.5	11.1	185	2	S52715		A;Genetics: C;Gene: Fasl
20	169.5	11.1	485	2	A33647		A;Introns: 151/1; 116/3
21	165.9	10.9	879	2	S27200		C;Keywords: glycoprotein; transmembrane protein
22	165	10.8	233	2	S11688		F;80-102/Domain: transmembrane #status predicted <TM>
23	163.5	10.7	234	1	JH0529		F;76, 184, 250, 260/Binding site: carbohydrate (Asn) (covalent) #status predicted
24	163	10.7	431	2	S47538		Query Match 10.0%; Score 1523; DB 2; Length 281;
25	162.5	10.7	1206	2	S24407		Best Local Similarity 100.0%; Pred. No. 1.2e-104;
26	162.5	10.7	1468	2	S11515		Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
27	161	10.6	193	2	S06192		tumor necrosis fac
28	160	10.5	235	2	I54490		tumor necrosis fac
29	159.5	10.5	511674				acrosin (EC 3.4.21 acrosin (EC 3.4.21
421	1	OY					formin isotorm IV formin - mouse

ALIGNMENTS

30	158.5	10.4	502	2	A55197		Wiskott-Aldrich syndrome tumor necrosis fac
31	157	10.3	235	1	QMSN		lymphotoxin-beta - glyceraldehyde-3-p
32	155.5	10.2	440	2	I49681		tumor necrosis fac hypothetical prote
33	155.5	10.1	235	2	JU0029		extensis homolog T hypothetical prote
34	154	10.1	708	2	D96711		nuclear protein EB cysteine-rich exte
35	153	10.0	760	2	T06291		chitinase (EC 3.2. regulatory protein unknown protein [I extensis - Volvox diaphanous protein hypothetical prote
36	152.5	10.0	1110	2	T19673		
37	152.5	10.0	487	2	S42442		
38	151	9.9	196	2	B48232		
39	151	9.9	439	2	S51939		
40	151	9.9	980	2	G86441		
41	151	9.9	1201	2	S22695		
42	151	9.9	464	2	T31057		
43	150.5	9.9	1255	2	A71416		
44	150.5	9.9	645	2			
45	149.5	9.8	645	2			

A;Molecule type: mRNA
A;Residues: 1-278 <SUD>
A;Cross-references: GB:U03470; NID:9440178; PID: AAC52129.1; PID:9440179
C;Keywords: glycoprotein; transmembrane protein

Query Match 74.6%; Score 1136.5; -DB 2; Length 278;
Best Local Similarity 76.6%; Pred. No. 2.8e-76; Gaps 3;
Matches 216; Conservative 21; Mismatches 40; Indels 5; Gaps 3;

QY 1 MQQPNNPYPOIYWDSASSPMPRGCTVIRCPYVPRRGQRPPPPPPPPP 60
Db 61 PPLPLPPLPLPKKRRNHSIGTCLLNFMLFLVALGGLGMFOLHLQELAELEESTSQ 120
61 PPLPLPPLPLPKKRRNHSIGTCLLNFMLFLVALGGLGMFOLHLQELAELEESTSQ 120
QY 121 MHTTASLEKQIGHSPPEKKERLKVAHITGKSNSRSRSMPLEWEDTYGIVLGSVYKKGG 180
Db 121 MHTTASLEKQIGHSPPEKKERLKVAHITGKSNSRSRSMPLEWEDTYGIVLGSVYKKGG 180
QY 181 LVINNETGLYFYSKYFGRGSCNNIPLSHKVMYMRNSKYPQLDVLMMEGKMSYCTGTQWMW 240
181 LVINNETGLYFYSKYFGRGSCNNIPLSHKVMYMRNSKYPQLDVLMMEGKMSYCTGTQWMW 240
QY 241 RSSYLGAVFNLTSAHDLYVNVSELSLVNFESQTFGLYKL 281
241 RSSYLGAVFNLTSAHDLYVNVSELSLVNFESQTFGLYKL 281

RESULT 2
A53062 ligand - mouse
Species: Mus musculus (house mouse)
Create: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: A53062
R;Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nagai, Cell 76, 969-976, 1994
A;Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in A;Reference number: A53062; NID:94185175; PMID:7511063
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-279 <TAG>
A;Cross-references: GB:U06948; NID:9473564; PIDN:AAA17800.1; PID:9473565
Query Match 75.9%; Score 1116; -DB 2; Length 279;
Best Local Similarity 77.3%; Pred. No. Ile-77; Matches 218; Conservative 25; Mismatches 35; Indels 4; Gaps 3;
QY 1 MQQPNNPYPOIYWDSASSPMPRGCTVIRCPYVPRRGQRPPPPPP-PLPLPPP 59
Db 1 MQQPNNPYPOQIFWDDSSATSSWAPPGSPFPCPGSPGPRQDRPPPPPVPSLPLPPSQ 60
QY 60 PPLPLPPLPLPKKGNHSIGTCLLNFMLFLVALGGLGMFOLHLQELAELEESTSQ 119
61 PLPLP-PLPLPKK-DHNINLWLWPLVFFKVLVALVGMLGMLGMLQFLHQELAELEFTN 116
QY 240 RSSYLGAVFNLTSAHDLYVNVSELSLVNFESQTFGLYKL 281
Db 237 AHSSYLGAVFNLTSAHDLYVNVSELSLVNFESQTFGLYKL 278

RESULT 4
JN0869 tumor necrosis factor beta - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
R;Kwon, J.; Chung, I.Y.; Benveniste, E.N.
Gene 132, 227-236, 1993
A;Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding gene
A;Reference number: JN0869; NID:94040766; PMID:8224868
A;Cross-references: GB:U00981; NID:9205253; PIDN:AAA16276.1; PID:9205255
A;Molecule type: DNA
A;Residues: 1-202 <RWO>
A;Accession: JN0869
A;Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding gene
A;Reference number: JN0868; NID:94040766; PMID:8224868
A;Molecule type: DNA
A;Residues: 1-202 <RWO>
A;Cross-references: GB:U00981; NID:9205253; PIDN:AAA16276.1; PID:9205255
A;Comment: Note: the authors translated codon CRC for residue 172 as Ile
C;Genetics:
A;Gene: TNF-beta
A;Introns: 32/7; 66/1
C;Superfamily: tumor necrosis factor
C;Keywords: tumor

Query Match 13.5%; Score 205; -DB 1; Length 202;
Best Local Similarity 32.9%; Pred. No. 4.2e-08; Matches 51; Conservative 27; Mismatches 67; Indels 10; Gaps 2;

QY 178 GLVINNETGLYFYSKYFGRGSCNNIPLSHKVMYMRNSKYPQLDVLMMEGKMSYCTGTQWMW 239
178 GLVINNETGLYFYSKYFGRGSCNNIPLSHKVMYMRNSKYPQLDVLMMEGKMSYCTGTQWMW 237
Db 240 ARSSYLGAVFNLTSAHDLYVNVSELSLVNFESQTFGLYKL 281
240 ARSSYLGAVFNLTSAHDLYVNVSELSLVNFESQTFGLYKL 281
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: A49266
A;Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor necrosis factor superfamily
A;Reference number: A49266; MUID:94084792; PMID:7505205
A;Status: preliminary

RESULT 3
A49266 fas ligand - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: A49266
A;Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor necrosis factor superfamily
A;Reference number: A49266; MUID:94084792; PMID:7505205
A;Status: preliminary

RESULT 5
B27303 tumor necrosis factor beta precursor - mouse
N;Alternative names: lymphotoxin; TNF beta

C;Species: *Mus musculus* (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 24-Sep-1999
C;Accession: B27303; S11342; S10083; 156004; 148853; 155980
R;Samon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhev, A.N.; Nedospasov, S.A.
Nucleic Acids Res. 15, 9083-9084, 1987

A;Reference number: 935679; MUID:88067722; PMID:3684584
A;Accession: B27303
A;Molecule type: DNA
A;Residues: 1-202 <SEM>
A;Cross-references: GB:X00467; NID:954830; PIDN:CAA68529_1; PID:954831
R;Nedospasov, S.A.; Hintz, B.; Shakhev, A.N.; Dobrynin, V.N.; Kawashima, E.; Accolla, R.S.
Nucleic Acids Res. 14, 7713-7725, 1986
A;Title: The genes for tumor necrosis factor (TNF-alpha) and lymphotoxin (TNF-beta) are
A;Reference number: S01342; MUID:87040736; PMID:3490653
A;Accession: S01342
A;Molecule type: DNA
A;Residues: 1-1139-1660, 'CG', 165-178 <NEED>
A;Cross-references: EMBL:X06217
R;Neil, D.; Daubert, F.
Onogene Res. 3, 409-414, 1988

A;Title: Induction of tumor necrosis factor-alpha and -beta and interferon-gamma mRNA by
A;Reference number: S10083; MUID:89144562; PMID:3147435
A;Accession: S10083
A;Molecule type: mRNA
A;Residues: 6-202 <WE1>
A;Cross-references: EMBL:X14800; PIDN:CAA32906_1; PID:9736269
R;Gardner, S.M.; Mock, B.A.; Higgers, J.; Huppi, K.E.; Reeder, W.D.
J. Immunol. 139, 476-483, 1987

A;Title: Mouse lymphotoxin and tumor necrosis factor: structural analysis of the cloned
A;Reference number: 156004; MUID:8722204; PMID:2885372
A;Accession: 156004
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Cross-references: GB:M17015; NID:9198880; PIDN:AA39450_1; PID:9387407
R;Gray, P.W.; Chen, E.; Li, C.B.; Tang, W.L.; Ruddle, N.
Nucleic Acids Res. 15, 3937, 1987
A;Title: The murine tumor necrosis factor-beta (lymphotoxin) gene sequence.
A;Reference number: 148853; MUID:87231097; PMID:3588316
A;Accession: 148853
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-202 <RE2>
A;Cross-references: EMBL:Y00137; NID:954842; PIDN:CAA68330_1; PID:954843
A;Title: Cloning and expression of murine lymphotoxin cDNA.
A;Reference number: 155980; MUID:87224127; PMID:2884262
A;Accession: 155980
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Residues: 1-202 <RE3>
A;Cross-references: GB:M16819; NID:9202088; PIDN:AAA40460_1; PID:9202089
A;Genes: Tnfb
C;Genetics: The first intron occurs in the 5'-untranslated region.
A;Map position: 17
A;Introns: 3/2/3; 66/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage

RESULT 6
JH0309
A;Cross-references: tumor necrosis factor beta precursor - rabbit
N;Alternate names: Lymphotoxin; TNF beta
C;Species: *Oryctolagus cuniculus* (domestic rabbit)
C;Accession: JH0309; PN0098
R;Shakhev, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
Gene 95, 215-221, 1990
A;Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF
A;Reference number: JH0309; MUID:91065534; PMID:2249779
A;Accession: JH0309
A;Molecule type: DNA
A;Residues: 1-197 <SH2>
A;Cross-references: GB:M60340; GB:M35326; NID:9165754; PIDN:AAA31483_1; PID:9165755;
R;Shakhev, A.N.; Kuprash, D.V.; Turetskaya, R.L.; Azizov, M.M.; Andreyeva, A.V.; Nedospasov, S.A.; Gardner, S.M.; Mock, B.A.; Higgers, J.; Huppi, K.E.; Reeder, W.D.
J. Immunol. 139, 476-483, 1987
A;Title: Cloning and structural analysis of the genes coding for rabbit tumor necrosis factor
A;Reference number: PN0098; MUID:90220566; PMID:2633043
A;Accession: PN0098
A;Residues: 1-197 <SHA>
A;Cross-references: GB:X55745; NID:9297167; PIDN:CAA39275_1; PID:9297168
A;Molecule type: mRNA
A;Accession: 1-197 <SH2>
C;Superfamily: tumor necrosis factor
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-197/Product: Lymphotoxin #status predicted <MAT>
A;Introns: 25/3; 61/1
A;Cross-references: GB:X55745; NID:9297167; PIDN:CAA39275_1; PID:9297168
A;Title: Cloning and expression of murine lymphotoxin cDNA.
A;Reference number: 155980; MUID:87224127; PMID:2884262
A;Accession: 155980
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Residues: 1-202 <RE3>
A;Cross-references: GB:M16819; NID:9202088; PIDN:AAA40460_1; PID:9202089
A;Genes: Tnfb
C;Genetics: The first intron occurs in the 5'-untranslated region.
A;Map position: 17
A;Introns: 3/2/3; 66/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage

RESULT 7
QWDX
Lymphotoxin alpha Precursor - human
N;Alternate names: Lymphotoxin A; TNF beta; tumor necrosis factor beta (TNF beta)
C;Species: *Homo sapiens* (man)
C;Date: 28-Aug-1998 #sequence_revision 07-Jul-1995 #text_change 16-Jun-2000
C;Accession: A92755; S36154; 154482; A93350; B32877; A91906; A61478; S26951; A01645;
R;Nedwin, G.E.; Jarrett-Nedin, J.; Smith, D.H.; Naylor, S.L.; Sakaguchi, A.Y.; Goeddel,
J. Cell. Biochem. 29, 171-181, 1985
A;Title: Structure and chromosomal localization of the human lymphotoxin gene.
A;Reference number: A92755; MUID:86086150; PMID:3001109
A;Accession: A92755
A;Molecule type: DNA
A;Residues: 1-59, 'N', 61-205 <NEED>
R;iris, F.J.M.; Bouquellet, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Ju
QY 191 VYSKVRERDQSCN-----NLPSHKVNRNSKVQDPLVMEKMSCTTGQWMARSSY 244
Db 106 VYSQVFSESCSPRAIPPIYLAHEVQLFQFLSSQYPFHVPLLSAQSKSVYFGLOPWFWSRY 165
Nature Genet. 3, 137-145, 1993

A;Title: Dense Alu clustering and a potential new member of the nkappaB family within a
A;Reference number: S36152; MUID:93272029; PMID:8499947
A;Accession: S36154
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-12, 'R' 14-205 <IRI>
A;Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78746.1; PID:g37213
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R;Abraham, L.J.; Du, D.C.; Zahedi, K.; Dawkins, R.L.; Whitehead, A.S.
Immunogenetics 33, 50-53, 1991
A;Title: Haplotype polymorphisms of the TNFB gene
A;Reference number: 154482; MUID:91139175; PMID:1671667
A;Accession: 154482
A;Status: translation not shown; translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-124, 'P' 126-205 <RES>
A;Cross-references: GB:M5913; NID:g339742; PIDN:AB859455.1; PID:g339743
A;Experimental source: ancestral haplotype 57.1
A;Note: 59 ASN was also found (ancestral haplotype 8.1)
R;GRAY, P.W.; Agarwal, B.B.; Benton, C.V.; Bringman, T.S.; Henzel, W.J.; Jarrett, J.A.;
Nature 312, 721-724, 1984
A;Title: Cloning and expression of cDNA for human lymphotoxin, a lymphokine with tumour
A;Reference number: A93350; MUID:85086243; PMID:6334807
A;Residue type: mRNA
A;Accession: B32877
A;Cross-references: GB:X01393; NID:934444; PIDN:CA25649.1; PID:g34445
A;Experimental source: lymphoblastoid cell line RPMI-1.88
R;Goeddel, D.V.; Agarwal, B.B.; Gray, P.W.; Leung, D.W.; Nedwin, G.E.; Palladino, M.A.;
Cold Spring Harb Symp. Quant. Biol. 51, 597-609, 1986
A;Title: Tumor necrosis factors: gene structure and biological activities.
A;Reference number: A32877; MUID:87217059; PMID:3472740
A;Accession: B32877
A;Cross-references: GB:00102; NID:0219913; PIDN:BA00064.1; PID:g219914
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 35-205 <GO>
R;Kobayashi, Y.; Miyamoto, D.; Asada, M.; Obinata, M.; Osawa, T.
J. Biochem. 100, 727-733, 1986
A;Title: Cloning and expression of human lymphotoxin mRNA derived from a human T cell hybridoma
A;Reference number: A91906; MUID:87057135; PMID:3536896
A;Accession: A91906
A;Molecule type: mRNA
A;Residues: 1-159, 'N' 61-205 <KOB>
A;Cross-references: GB:D00102; NID:0219913; PIDN:BA00064.1; PID:g219914
A;Note: the authors translated the codon TAT for residue 156 as Thr and ACC for residue 157 as Tyr.
R;Fukuda, S.; Ando, S.; Sanou, O.; Tanai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; An
Lymphokine Res. 7, 175-185, 1988
A;Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and
A;Reference number: A61478; MUID:88301617; PMID:2841543
A;Accession: A61478
A;Molecule type: protein
A;Cross-references: GB:00102; NID:0219913; PIDN:BA00064.1; PID:g219914
A;Residues: 56-79, 86-95, 'X', 97, 'X', 99, 119-151, 'XX', 154-162, 'X', 164, 'X', 166, 'X', 168, 'X', 1
R;Hoigt, C.G.; Maurer-Fogy, I.; Adolf, G.R.
IEBS Lett. 314, 85-88, 1992
A;Title: Natural human tumor necrosis factor beta (lymphotoxin). variable O-glycosylation
A;Reference number: S26951; MUID:93083656; PMID:1451807
A;Molecule type: protein
A;Accession: S26951
A;Cross-references: GB:00102; NID:0219913; PIDN:BA00064.1; PID:g219914
A;Residues: 35-59, 'N', 61-205 <VOI>
A;Note: 60-Thr was also found
R;Fukushima, K.; Watson, H.; Takeo, K.; Nomura, M.; Asahi, T.; Yamashita, K.
Arch. Biochem. Biophys. 304, 14-153, 1993
A;Title: N-linked sugar chain structure of recombinant human lymphotoxin produced by CHO
A;Reference number: S34742; MUID:93311995; PMID:8232280
A;Contents: annotation
C;Comment: Secreted from mitogen-activated lymphocytes within 1-2 days after induction, while having no detrimental effect on normal cells. It can also act synergistically with TNF-alpha (tumor necrosis factor) are the products of different induction kill
C;Comment: This protein and TNF-alpha (tumor necrosis factor) are the products of different induction kill
A;Cross-references: GDB:110442; OMIM:153440
A;Map position: 6p21.3-5p21.3

Query Match 12.5%; Score 186.5; DB 1; Length 234;
Best Local Similarity 27.2%; Pred. No. 1,1e-06;
Matches 62; Conservative 36; Mismatches 99; Indels 31; Gaps 10;
QY 72 KKRGENHSQGCLLVMFFNLVALWLGIGMFOLHL-----OKELAELRESTSQHTA 124
Db 19 LLLGLLVLVLPQAGQGPVGV-----LTPSAQTAROHPKHLHS----- 59
QY 140 KKEILRKVHLTGKGSNSRSMPLMEDTGVILISGVKVKGGLVINETGLYFVSKYFRG 199
Db 60 --TILKPAHLIGPKSQNSLNRANTDRAFLQDGESLSNSLIVPISGIVYPSQVFG 117
QY 200 Q-----SCNNPLSHKYMRSKYPDLVMMEGKMSYCCTGQMWARSSYLVAVNUTS 253
Db 118 KAYSPPKATSSPPLYLAHEVQLFSSQIPFIVPLLSSQKAVYPGQCEPWHSMWIGAQALQ 177
QY 254 ADHLYVNVYSELVNFEEQSOTFGLYKL 281
Db 178 GDQLSTHTDGIPHLVLSPTVFGAFAL 205

RESULT 8

J01344 tumor necrosis factor alpha precursor - horse
N;Alternate names: cachectin; TNF alpha
C;Species: Equus caballus (domestic horse)
C;Date: 10-Sep-1999 #sequence_revision
C;Accession: J01344
R;Su, X.; Morris, D.D.; Mcgraw, R.A.
Gene 107, 319-321, 1991
A;Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis factor
A;Reference number: J01344; MUID:92084125; PMID:148301
A;Accession: J01344
A;Molecule type: DNA
A;Residues: 1-234 <SUX>
A;Cross-references: GB:M64087; NID:9164244; PIDN:AAA30959.1; PID:9164245
C;Comment: This protein is an important proximal mediator of endotoxemia.
C;Genetics:
A;Gene: TNF-alpha
A;Introns: G2/3; 79/1; 95/1
A;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m
F19, 20/Binding site: tumor necrosis factor alpha #status predicted
F19, 20/Binding site: myristate (Lys) (covalent) #status predicted
F182/Binding site: carbohydrate (Ser) (covalent) #status predicted
F146-178/disulfide bonds: #status predicted

Query Match 12.5%; Score 186.5; DB 1; Length 234;
Best Local Similarity 27.2%; Pred. No. 1,1e-06;
Matches 62; Conservative 36; Mismatches 99; Indels 31; Gaps 10;
QY 72 KKRGENHSQGCLLVMFFNLVALWLGIGMFOLHL-----OKELAELRESTSQHTA 124
Db 20 KAGGPQGSRRCILSFSFL-LVAGANTLCECLLHRFGVIGPOREELQPNATOSINPL-A 75
QY 125 SSLEKQICGHPSPEPKERLKVAHLTGKGSNSRSMPLMEDTGVILISGVKVKGGLV 183
Db 76 QTRSSRTSPSKP-----VAHWVNPQASQ-LQWSGRANALLANGVLLWV 127
QY 184 NETGLYVYSKYFVFGOSC--NNLPLSHKYMRSKYPDLVMMEGKMSYCCTGQMWARSSYLVAVNUTS 235
Db 128 PLDGLYLISQVLFKGCGCPSTVHLTISLAVSIPSQSKVNLSA-IKSPCHTESPEQA 186
QY 236 -GOMARASSYIYGAVNTSDAHLYVNVYSELVNFEEQSOTFGLYKL 281

Db 187 EAKPQYEPPIVLLGGVFOLEKGDOLSAEINQNYLDFAESGOVYFGIIL 234
 RESULT 9
 S12606 tumor necrosis factor alpha precursor - pig
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
 C;Accession: S12606; S1290; S18965; 146659
 R;Drews, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.
 Nucleic acids Res. 18, 5564, 1990
 A;Title: Gene sequence of porcine tumor necrosis factor alpha.
 A;Reference number: S12606; MUID:91016861; PMID:2216741
 A;Accession: S12606
 A;Molecule type: DNA
 A;Residues: 1-232 <DRE>
 A;Cross-references: EMBL:X54001; NID:92135; PIDN:CAA37949.1; PID:92136
 R;Kuhnert, P.; Wuetrich, C.; Peterhans, E.; Pauli, U.
 Gene 102, 171-178, 1991
 A;Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative analysis
 A;Reference number: S17289; MUID:91340150; PMID:187444
 A;Accession: S17290
 A;Molecule type: DNA
 A;Residues: 1-232 <KUH>
 A;Cross-references: EMBL:X54859; NID:92132; PIDN:CAA38639.1; PID:92134
 A;Note: the authors translated the codon GAG for residue 202 as GLY
 R;Choi, C.S.; Molitor, T.W.; Lin, G.F.; Murtaugh, M.P.
 submitted to the EMBL Data Library, January 1991
 A;Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis factor
 A;Reference number: S18965
 A;Accession: S18965
 A;Molecule type: mRNA
 A;Residues: 1-232 <CHO>
 A;Cross-references: EMBL:X57321; NID:92137; PIDN:CAA40591.1; PID:92138
 R;Pauli, U.; Beutler, B.; Peterhans, E.
 Gene 81, 185-191, 1989
 A;Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain reaction
 A;Accession: I46659
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 44-232 <PAU>
 A;Cross-references: GB:M9079; NID:9164694; PIDN:AAA31128.1; PID:9164695
 QY 130 QIGHSPSPPE--KKELRKVAHITGKNSNSRSMPLWE-DTIGIVLISVGKVKKGGVINE 186
 Db 45 OPAHQPKHARGTLPKAHNGWDSTP-SLRRAAFTDRAFTLRRGLFNNNSLWPT 103
 R;C;Superfamily: tumor necrosis factor
 C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage
 F;1-77/Domain: propeptide #status predicted <PRO>
 F;78-232/Product: tumor necrosis factor alpha #status predicted <MAT>
 F;19-20/Binding site: myristate (lys) (covalent) #status predicted
 F;18/Binding site: carbohydrate (ser) (covalent) #status predicted
 F;144-176/disulfide bonds: #status predicted
 Query Match 12-18; Score 184; DB 1; Length 204;
 Best Local Similarity 32.7%; Pred. No. 1.5e-06; Matches 53; Conservative 22; Mismatches 75; Indels 12; Gaps 6;
 Db 187 GLYFVVSKVYFRGQC-----NNPLSHKVYMRNSKYPQLVMMEGKMMMSYCTGQ-MW 239
 QY 104 GLYFVVISQVVSFGEGCFPKAPTPYLAEVQFLSSQYFVAVPLSAQ-KSVCPSPQGPW 162
 Db 240 ARSSYGAVENTLSAHLVNVNSELVNEFESQTSQFLGYKL 281
 Db 163 VRSVYOGAVELLTQGDOLSTHTDGTPHILLSPSSVFFGAFAL 204
 RESULT 11
 S24641 lymphotoxin - bovine.
 C;Species: Bos primigenius taurus (cattle).
 C;Date: 10-Sep-1999 #sequence_revision 10-sep-1999
 C;Accession: I46046; S24641
 R;Cluets, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
 Cytokine 5, 336-341, 1993
 A;Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and
 A;Reference number: I46046; MUID:94083525; PMID:8260599
 A;Accession: I46046
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-204 <CL2>
 A;Cross-references: EMBL:Z14137; NID:9796; PIDN:CAA78510.1; PID:9797
 C;Genetics:
 C;Introns: 32/3; 68/1
 C;Superfamily: tumor necrosis factor
 Query Match 12-28; Score 185.5; DB 1; Length 232;
 Best Local Similarity 28.7%; Pred. No. 1.3e-06; Matches 68; Conservative 26; Mismatches 92; Indels 51; Gaps 10;
 Db 72 KKRGNHSTGLCLLVMFFMVNLVALVGLGMQLFHL----QKE-----LAELR 115
 QY 1 20 KAGPGQSRRLCLSLFSFL-LVAGATLFCLLREVIGQKEEPAGPLSINPLAQL 77
 Db 116 ESTSQMTTASSLEKQIGHPSPPEKKELRKVAHITGKNSNSRSMPLWE-DTIGIVLISVG 174
 QY 1 78 RSSQTSR-----KPAHVANVKAEGQ-LQWQSGYANALLANGV 116
 QY 175 KYKGGSIVINPTGLYEVSKYFQSC--NNLPSPHKVYMRNSKYPQLDVTMEGRMSY 232
 Db 117 KIKDNQLVPTDGLYLYISQVLFRGCGPSNTVFLHTSIVLAVS-QTKVNLLSAIKSP 175
 QY 233 C-----TTGOMWARSSYLGAVPNITSADHLYLVNSELVNFEESSQFGLYKL 281
 Db 176 CORETPGAAEAKPWPYPIVLLGGVFOLEKDRDLSAFEINLPDYLDAESGQVYFGIIL 232
 Query Match 12-28; Score 183.5; DB 1; Length 204;
 Best Local Similarity 31.5%; Pred. No. 1.6e-06; Matches 62; Conservative 27; Mismatches 89; Indels 19; Gaps 8;
 Db 94 LVGLGIGMFQLFPHIQKELAELRESTSQMTTASSLEKQIGHPSPPEKKELRKVAHITGK 152
 Db 18 LILIGL---LIALPLAQAQIGRIGKIGLTPSAAQPOHQL---PTPPTGRTQPKPAHLVG 69
 QY 153 SNRSMPLWE-DTIGIVLISVGKVYKKGGVINEIGLYFVSKVFRGQC-----NNL 205
 Db 70 PSTQD-SLRWRANTDRAFTLRRGIFSLNSLNLSVPTGFLYFVSOVFSGRGCPRPTPL 128
 QY 206 PLSKVYMRNSKYPQLDVTMEGRMSYLGAVPNITSADHLYLVNSELVNFEESSQFGLYKL 264

RESULT 12

S24642 tumor necrosis factor alpha precursor - bovine

C;Species: Bos primigenius taurus (cattle)

C;Accession: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

R;Clouds, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Drogmans, L.

Cytokine 5, 336-341, 1993

A;Title: Cloning and characterization of the tandemly arranged bovine lymphotaxin and tumor necrosis factor genes

A;Reference number: I46046; MUID:94083525; PMID:8260599

A;Accession: I46047

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-233 <CL2>

A;Cross-references: EMBL:214137; NID:9796; PIDN:CAA78511.1; PID:9798

C;Genetics: INFA

A;Introns: 62/3; 78/1; 94/1

C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F;2/Binding site: myristate (Lys) (covalent) #status predicted

F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F;145-177/Disulfide bonds: #status predicted

Query Match Best Local Similarity 29.4%; Pred. No. 2e-06; Matches 65; Conservative 27; Mismatches 11; Indels 18; Gaps 8;

Qy 72 KKRGNHSTGCLLIVMFVFLVALVGLGIGMFQLEFHQLKELAEURETSQSOMHASSLKQI 131

Db 20 KAGCOPQGSRSCILSLSFL-LVAGATPLFCILHFVGIVPGORESPCGPSINSPLVOTL 77

Qy 132 GHSPPPKEKKERLVKAHLTGKSNRSRSMPLIEDTYGIVL-SGVYKKGLVNETGLF 190

Db 78 RSSQASSNK--PVAHYWADINSPGQ-LRWMDSYANALMANGVKLDNQLVYPADGLYI 133

Qy 191 VYSKVYFRGOSCNMLP-LISKVYMRNSRKYPODULMMGGKMMSC-----TTGQWAPR 241

Db 134 IVSQVLFRQGCGPSTPLFLHTISRIAVS-QTKVNILSAIKSPCHRETPPEAEPKWE 192

Qy 242 SSVLAGAVNLTSADHLYVNVSELSVLYNEES-OTFGGLYKL 281

Db 193 PIYQGGVFRQLEKGDRSLAEINLPDYDVAESGOVYFGITAL 233

RESULT 13

S24642 tumor necrosis factor alpha precursor [validated] - human

N;Alternate names: cachectin; TNFA

C;Species: Homo sapiens (man)

C;Accession: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Dec-2000

R;Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D.

Nucleic Acids Res. 13, 6361-6373, 1985

A;Title: Human lymphotaxin and tumor necrosis factor genes: structure, homology and chrc

A;Reference number: A93585; MUID:86016093; PMID:2995927

A;Accession: A93585

A;Molecule type: DNA

A;Residues: 1-233 <NE>

A;Cross-references: GB:X02010; GE:X02159; NID:37200; PIDN:CAA26660.1; PID:937210

R;Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka, Nature Genet 3, 137-145, 1993

A;Title: Dense Alu clustering and a potential new member of the NFkappaB family within a

A;Reference number: S36152; MUID:93272029; PMID:849947

A;Accession: S36153

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-233 <IR>

A;Cross-references: EMBL:215026; NID:937211; PIDN:CAA78745.1; PID:937210

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992

R;Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seburg, P.H.; Deryck, R.; Palladino, M. Nature 312, 724-729, 1984

A;Title: Human tumour necrosis factor: precursor structure, expression and homology to TNF

A;Reference number: A93351; MUID:85086244; PMID:6392892

A;Accession: A93351

A;Molecule type: mRNA

A;Residues: 1-233 <PE>

A;Cross-references: GB:X02910; GB:X02159; NID:937209; PIDN:CAA26669.1; PID:937210

A;Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyelocytic leukaemia cell line. It has been shown to be identical to TNF

R;Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Asdell, J.N. Science 228, 149-154, 1985

A;Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.

A;Reference number: AA4189; MUID:85142190; PMID:3856324

A;Accession: AA4189

A;Molecule type: mRNA

A;Residues: 1-62, S, 64-233 <WAN>

A;Cross-references: GB:M10988; NID:9339737; PIDN:AAA61198.1; PID:933938

R;Fukuda, S.; Ando, S.; Samou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; Lymphokine Res. 7, 175-185, 1988

Eur. J. Biochem. 152, 515-522, 1985

A;Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and -gamma

A;Reference number: A61478; MUID:88301617; PMID:2841543

A;Accession: B61478

A;Molecule type: Protein

A;Residues: 83-102; 109-119; 121-128, X', 130-131; 142-144, X', 146, 'XXX', 150-152; 159-174; R;Marmenot, A.; Franzen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima Eur. J. Biochem. 152, 515-522, 1985

A;Title: Molecular cloning and expression of human tumor necrosis factor-alpha, -beta and -gamma

A;Reference number: I53311; MUID:86030296; PMID:3932069

A;Accession: I53311

A;Status: translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Reference number: 153311; MUID:96202967; PMID:8631363

A;Accession: S62610

A;Cross-references: GB:M26331; NID:9339763; PIDN:AAA36758.1; PID:9339764

A;Experimental source: U-937 cells

R;Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.

Eur. J. Biochem. 235, 431-437, 1996

A;Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.

A;Reference number: 39, 150-154, 1994

A;Accession: S62610

A;Molecule type: protein

A;Residues: 77-99 <TAK>

R;Alfonso, S.; Richard, P.M.

Immunogenetics 39, 150-154, 1994

A;Title: A polymorphic variation in a putative regulation box of the TNFA promoter region

A;Reference number: 154522; MUID:94102809; PMID:7903959

A;Accession: I54522

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-8 <DA>

A;Cross-references: GB:S68530; NID:9544751

R;Stevenson, P.R.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.

J. Exp. Med. 176, 1053-1062, 1992

A;Title: Myristylation of the tumor necrosis factor alpha precursor on specific amino acids

A;Reference number: A59163; MUID:93018820; PMID:1402651

A;Contents: annotation; identification of myristylated lysines

R;Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Br J. Biol. Chem. 260, 2235-2234, 1985

A;Title: Human tumor necrosis factor. Production, purification, and characterization.

A;Reference number: A92511; MUID:85130974; PMID:3871770

A;Contents: annotation; disulfide bond

A;Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induction. It can also act synergistically with interferon gamma to stimulate TNF

C;Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes closely related to TNF. They are produced by different cell types and have different induction kinetics.

C;Genetics:

A;Gene: GDB:TNF; TNFA

A;Cross-references: GDB:120441; OMIM:191160

A;Map position: 6p21.3-6p21.3

A;Introns: 62/3; 78/1; 94/1

C; Complex: homotrimer
 C; Superfamily: tumor necrosis factor
 C; Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; macrophage; myristylation; transmembrane protein
 F; 11/16/Domain: propeptide #status predicted <PRO>
 F; 77-233/Product: tumor necrosis factor #status experimental <MAT>
 F; 81/Binding site: myristate (Lys) (covalent) #status experimental
 F; 145-177/Disulfide bonds: #status experimental
 Query Match 11.9%; Score 181; DB 1; Length 233;
 Best Local Similarity 27.4%; Pred. No. 2. 9e-06; Mismatches 112; Indels 18; Gaps 8;
 Matches 61; Conservative 32; Mismatches 112; Indels 18; Gaps 8;
 Qy 70 PLKKRGHNSHTGCLLVMFEMVIALVGLGLMFOFLHQKELAELRESTSQMTTASLEK 129
 Db 18 PRKTGGPQGSRRCFLSLSFLI--VAGATTFLCILHFGVIGPQREFPDLISPLAQ 75
 Qy 130 QIGHPSPPPEKKERLKVKVAHLGCKNSNSRNSMPLMEDTYGIVIL-SGVYKKGGLVINTGL 188
 Db 76 AVRSSSRPDSK--PVAVHVVANPOABQ-LQWLNRRANALLANGVVELRDNOQLUVPSEG 131
 Qy 189 YFVYSKVFGRGSC--NNPLSIKVYMRNSKVPDLVMEGRMSYC-----TCQMW 239
 Db 132 YLYSQVLFKGOGCPSTHVLLHTISRAVSY-OTKVNLLSAIKSPCORETPEGAEAKPW 190
 Qy 240 ARSSYLGAVFNLTSDADLVNVNSELVNFES-QTFFGGLYKL 281
 Db 191 YEPYLGGVFOLEKGDRLSAEINRPDYLDAESGQVYFGGIAL 233
 RESULT 14
 A34043
 hypothetical proline-rich protein 1 - polychaete (*Owenia fusiformis*) (fragment)
 C; Species: *Owenia fusiformis*
 C; Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 01-Dec-2000
 C; Accession: A34043; B34043
 R; Bakalar, N.; Collet, J.; Planells, R.; Thouveny, Y.; Fontes, M.
 R; Bakalar, N.; Collet, J.; Planells, R.; Thouveny, Y.; Fontes, M.
 R; Bakalar, N.; Collet, J.; Planells, R.; Thouveny, Y.; Fontes, M.
 R; Bakalar, N.; Collet, J.; Planells, R.; Thouveny, Y.; Fontes, M.
 A; Title: Presence in invertebrate genomes of sequences characterized by the repetition of
 A; Reference number: A90159; MUID: 90147742; PMID: 2105723
 A; Accession: A34043
 A; Molecule type: DNA
 A; Residues: 1-141 <B&H>
 A; Cross-references: GB:M32217
 A; Accession: B34043
 A; Molecule type: DNA
 A; Residues: 59-136 <B&H>
 A; Cross-references: GB:M32217
 Query Match 11.6%; Score 177; DB 2; Length 141;
 Best Local Similarity 49.3%; Pred. No. 3. 2e-06; Mismatches 28; Indels 2; Gaps 1;
 Matches 35; Conservative 6; Mismatches 28; Indels 2; Gaps 1;
 Qy 18 SASSPPWPAGTVLPCPTSVPRPGQRREPPPPPPPLPPPPPLPPLPLPPLKKRGNH 77
 Db 6 SLTPPPRRARIH 65
 Qy 78 STGICLUMNFE 88
 Db 66 N--IPLERREF 74
 RESULT 15
 S22052
 tumor necrosis factor alpha precursor - baboon
 C; Species: *Papio sp.* (baboon)
 C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
 C; Accession: S22052
 R; Sanjanwala, M.; Edwards, A.
 submitted to the EMBL Data Library, September 1991
 A; Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.
 A; Reference number: S22052
 A; Accession: S22052

A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-233 <SAN>
 A; Cross-references: EMBL:X62141; NID:938159; PID:938160
 C; Genetics:
 A; Introns: 62/3; 78/1; 94/1
 C; Superfamily: tumor necrosis factor
 C; Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
 F; 19-20/Binding site: myristate (Lys) (covalent) #status predicted
 F; 81/Binding site: myristate (Lys) (covalent) #status experimental
 F; 145-177/Disulfide bonds: #status predicted
 Query Match 11.6%; Score 176; DB 1; Length 233;
 Best Local Similarity 27.8%; Pred. No. 6. 7e-06; Mismatches 113; Indels 18; Gaps 8;
 Matches 62; Conservative 30; Mismatches 113; Indels 18; Gaps 8;
 Qy 70 PLKKRGHNSHTGCLLVMFEMVIALVGLGLMFOFLHQKELAELRESTSQMTTASLEK 129
 Db 18 PPKTGGPQGSRRCFLSLSFLI--VAGATTFLCILHFGVIGPQREFPDLISPLAQ 75
 Qy 130 QIGHPSPPPEKKERLKVKVAHLGCKNSNSRNSMPLMEDTYGIVIL-SGVYKKGGLVINTGL 188
 Db 76 AVRSSSRPDSK--PVAVHVVANPOABQ-LQWLNRRANALLANGVVELRDNOQLUVPSEG 131
 Qy 189 YFVYSKVFGRGSC--NNPLSIKVYMRNSKVPDLVMEGRMSYC-----TCQMW 239
 Db 132 YLYSQVLFKGOGCPSTHVLLHTISRAVSY-OTKVNLLSAIKSPCORETPEGAEAKPW 190
 Qy 240 ARSSYLGAVFNLTSDADLVNVNSELVNFES-QTFFGGLYKL 281
 Db 191 YEPYLGGVFOLEKGDRLSAEINRPDYLDAESGQVYFGGIAL 233
 Search completed: June 24, 2003, 11:08:51
 Job time : 22.350 secs

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